

## SEQUENCE LISTING

## (1) GENERAL INFORMATION:

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## (i) APPLICANT:

- (A) NAME: DANISCO A/S
- (B) STREET: Langebrogade 1
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- (F) POSTAL CODE (ZIP): 1001 K
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- (ii) TITLE OF INVENTION: Cloning and use of Lipase 3 gene from *Aspergillus tubigensis*

- (iii) NUMBER OF SEQUENCES: 9

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## (iv) COMPUTER READABLE FORM:

- (A) MEDIUM TYPE: Floppy disk
- (B) COMPUTER: IBM PC compatible
- (C) OPERATING SYSTEM: PC-DOS/MS-DOS
- (D) SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)

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## (2) INFORMATION FOR SEQ ID NO: 1:

## (i) SEQUENCE CHARACTERISTICS:

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- (A) LENGTH: 25 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

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- (ii) MOLECULE TYPE: peptide

- (v) FRAGMENT TYPE: N-terminal

## (vi) ORIGINAL SOURCE:

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- (A) ORGANISM: *Aspergillus tubigensis*

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

Ser Val Ser Thr Ser Thr Leu Asp Glu Leu Gln Leu Phe Ala Gln Trp  
 1 5 10 15

Ser Ala Ala Ala Tyr Xaa Ser Asn Asn  
 20 25

(2) INFORMATION FOR SEQ ID NO: 2:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 7 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: internal

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Aspergillus tubigensis*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

Val His Thr Gly Phe Trp Lys  
 1 5

(2) INFORMATION FOR SEQ ID NO: 3:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 14 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: internal

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Aspergillus tubigensis*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

Ala Trp Glu Ser Ala Ala Asp Glu Leu Thr Ser Lys Ile Lys  
 5        1                                5                                10

(2) INFORMATION FOR SEQ ID NO: 4:

(i) SEQUENCE CHARACTERISTICS:

10        (A) LENGTH: 20 base pairs  
           (B) TYPE: nucleic acid  
           (C) STRANDEDNESS: single  
           (D) TOPOLOGY: linear

15        (ii) MOLECULE TYPE: other nucleic acid

          (A) DESCRIPTION: /desc = "Oligonucleotide"

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

TTCCARAANC CNGTRTGNAC

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25 (2) INFORMATION FOR SEQ ID NO: 5:

(i) SEQUENCE CHARACTERISTICS:

30        (A) LENGTH: 18 base pairs  
           (B) TYPE: nucleic acid  
           (C) STRANDEDNESS: single  
           (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "Oligonucleotide"

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

40

CARYTNTTYG CNCARTGG

18

(2) INFORMATION FOR SEQ ID NO: 6:

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(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 17 base pairs

(B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

5 (ii) MOLECULE TYPE: other nucleic acid  
 (A) DESCRIPTION: /desc = "Oligonucleotide"

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

GCVGCHSWYT CCCAVGC

17

15 (2) INFORMATION FOR SEQ ID NO: 7:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 317 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

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(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "PCR fragment"

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

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CAGTTGTTTCG CGCAATGGTC TGCCGCAGCT TATTGCTCGA ATAATATCGA CTCGAAAGAV 60

TCCAACCTTGA CATGCACGGC CAACGCCTGT CCATCAGTCG AGGAGGCCAG TACCACGATG 120

35 CTGCTGGAGT TCGACCTGTA TGTCACCTCAG ATCGCAGACA TAGAGCACAG CTAATTGAAC 180

AGGACGAACG ACTTTTGGAG GCACAGCCGG TTTCCTGGCC GCGGACAACA CCAACAAGCG 240

GCTCGTGGTC GCCTTCCGGG GAAGCAGCAC GATTGAGAAC TGGATTGCTA ATCYTGACTT 300

40

CATCCTGGRA GATAACG

317

(2) INFORMATION FOR SEQ ID NO: 8:

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(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1045 base pairs

(B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

5 (ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Aspergillus tubigensis*

10 (ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: join(1..82, 135..300, 347..683, 737..1045)

(ix) FEATURE:

15 (A) NAME/KEY: sig\_peptide

(B) LOCATION: 1..81

(ix) FEATURE:

(A) NAME/KEY: mat\_peptide

20 (B) LOCATION: join(82, 135..300, 347..683, 737..1042)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

25	ATG TTC TCT GGA CGG TTT GGA GTG CTT TTG ACA GCG CTT GCT GCG CTG	48
	Met Phe Ser Gly Arg Phe Gly Val Leu Leu Thr Ala Leu Ala Ala Leu	
	-27        -25                                -20                                -15	
	GGT GCT GCC GCG CCG GCA CCG CTT GCT GTG CGG A GTAGGTGTGC	92
30	Gly Ala Ala Ala Pro Ala Pro Leu Ala Val Arg	
	-10    -5	
	CCGATGTGAG ATGGTTGGAT AGCACTGATG AAGGGTGAAT AG GT GTC TCG ACT	145
		Ser Val Ser Thr
35		1
	TCC ACG TTG GAT GAG TTG CAA TTG TTC GCG CAA TGG TCT GCC GCA GCT	193
	Ser Thr Leu Asp Glu Leu Gln Leu Phe Ala Gln Trp Ser Ala Ala Ala	
	5    10    15    20	
40	TAT TGC TCG AAT AAT ATC GAC TCG AAA GAC TCC AAC TTG ACA TGC ACG	241
	Tyr Cys Ser Asn Asn Ile Asp Ser Lys Asp Ser Asn Leu Thr Cys Thr	
	25    30    35	
45	GCC AAC GCC TGT CCA TCA GTC GAG GAG GCC AGT ACC ACG ATG CTG CTG	289
	Ala Asn Ala Cys Pro Ser Val Glu Glu Ala Ser Thr Thr Met Leu Leu	

	40	45	50	
	GAG TTC GAC CT	GTATGTCACT CAGATCGCAG	ACATAGAGCA CAGCTAATTT	340
	Glu Phe Asp Leu			
5	55			
	GAACAG G ACG AAC GAC TTT GGA GGC ACA GCC GGT TTC CTG GCC GCG GAC			389
	Thr Asn Asp Phe Gly Gly Thr Ala Gly Phe Leu Ala Ala Asp			
	60	65	70	
10				
	AAC ACC AAC AAG CGG CTC GTG GTC GCC TTC CGG GGA AGC AGC ACG ATT			437
	Asn Thr Asn Lys Arg Leu Val Val Ala Phe Arg Gly Ser Ser Thr Ile			
	75	80	85	
15	GAG AAC TGG ATT GCT AAT CTT GAC TTC ATC CTG GAA GAT AAC GAC GAC			485
	Glu Asn Trp Ile Ala Asn Leu Asp Phe Ile Leu Glu Asp Asn Asp Asp			
	90	95	100	
	CTC TGC ACC GGC TGC AAG GTC CAT ACT GGT TTC TGG AAG GCA TGG GAG			533
20	Leu Cys Thr Gly Cys Lys Val His Thr Gly Phe Trp Lys Ala Trp Glu			
	105	110	115	
	TCC GCT GCC GAC GAA CTG ACG AGC AAG ATC AAG TCT GCG ATG AGC ACG			581
	Ser Ala Ala Asp Glu Leu Thr Ser Lys Ile Lys Ser Ala Met Ser Thr			
25	120	125	130	
	TAT TCG GGC TAT ACC CTA TAC TTC ACC GGG CAC AGT TTG GGC GGC GCA			629
	Tyr Ser Gly Tyr Thr Leu Tyr Phe Thr Gly His Ser Leu Gly Gly Ala			
	135	140	145	150
30				
	TTG GCT ACG CTG GGA GCG ACA GTT CTG CGA AAT GAC GGA TAT AGC GTT			677
	Leu Ala Thr Leu Gly Ala Thr Val Leu Arg Asn Asp Gly Tyr Ser Val			
	155	160	165	
35	GAG CTG GTGAGTCCTT CACAAAGGTG ATGGAGCGAC AATCGGGAAC AGACAGTCAA			733
	Glu Leu			
	TAG TAC ACC TAT GGA TGT CCT CGA ATC GGA AAC TAT GCG CTG GCT GAG			781
40	Tyr Thr Tyr Gly Cys Pro Arg Ile Gly Asn Tyr Ala Leu Ala Glu			
	170	175	180	
	CAT ATC ACC AGT CAG GGA TCT GGG GCC AAC TTC CGT GTT ACA CAC TTG			829
	His Ile Thr Ser Gln Gly Ser Gly Ala Asn Phe Arg Val Thr His Leu			
45	185	190	195	

AAC GAC ATC GTC CCC CGG GTG CCA CCC ATG GAC TTT GGA TTC AGT CAG 877  
 Asn Asp Ile Val Pro Arg Val Pro Pro Met Asp Phe Gly Phe Ser Gln  
 5 200 205 210 215

CCA AGT CCG GAA TAC TGG ATC ACC AGT GGC AAT GGA GCC AGT GTC ACG 925  
 Pro Ser Pro Glu Tyr Trp Ile Thr Ser Gly Asn Gly Ala Ser Val Thr  
 220 225 230

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GCG TCG GAT ATC GAA GTC ATC GAG GGA ATC AAT TCA ACG GCG GGA AAT 973  
 Ala Ser Asp Ile Glu Val Ile Glu Gly Ile Asn Ser Thr Ala Gly Asn  
 235 240 245

15 GCA GGC GAA GCA ACG GTG AGC GTT GTG GCT CAC TTG TGG TAC TTT TTT 1021  
 Ala Gly Glu Ala Thr Val Ser Val Val Ala His Leu Trp Tyr Phe Phe  
 250 255 260

GCG ATT TCC GAG TGC CTG CTA TAA 1045  
 20 Ala Ile Ser Glu Cys Leu Leu \*  
 265 270

## (2) INFORMATION FOR SEQ ID NO: 9:

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## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 297 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

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(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:

Met Phe Ser Gly Arg Phe Gly Val Leu Leu Thr Ala Leu Ala Ala Leu  
 35 -27 -25 -20 -15

Gly Ala Ala Ala Pro Ala Pro Leu Ala Val Arg Ser Val Ser Thr Ser  
 -10 -5 1 5

40 Thr Leu Asp Glu Leu Gln Leu Phe Ala Gln Trp Ser Ala Ala Ala Tyr  
 10 15 20

Cys Ser Asn Asn Ile Asp Ser Lys Asp Ser Asn Leu Thr Cys Thr Ala  
 25 30 35

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Asn Ala Cys Pro Ser Val Glu Glu Ala Ser Thr Thr Met Leu Leu Glu

40                      45                      50  
 Phe Asp Leu Thr Asn Asp Phe Gly Gly Thr Ala Gly Phe Leu Ala Ala  
     55                      60                      65  
 5  
 Asp Asn Thr Asn Lys Arg Leu Val Val Ala Phe Arg Gly Ser Ser Thr  
     70                      75                      80                      85  
 Ile Glu Asn Trp Ile Ala Asn Leu Asp Phe Ile Leu Glu Asp Asn Asp  
 10                      90                      95                      100  
 Asp Leu Cys Thr Gly Cys Lys Val His Thr Gly Phe Trp Lys Ala Trp  
                     105                      110                      115  
 15 Glu Ser Ala Ala Asp Glu Leu Thr Ser Lys Ile Lys Ser Ala Met Ser  
                     120                      125                      130  
 Thr Tyr Ser Gly Tyr Thr Leu Tyr Phe Thr Gly His Ser Leu Gly Gly  
     135                      140                      145  
 20  
 Ala Leu Ala Thr Leu Gly Ala Thr Val Leu Arg Asn Asp Gly Tyr Ser  
     150                      155                      160                      165  
 Val Glu Leu Tyr Thr Tyr Gly Cys Pro Arg Ile Gly Asn Tyr Ala Leu  
 25                      170                      175                      180  
 Ala Glu His Ile Thr Ser Gln Gly Ser Gly Ala Asn Phe Arg Val Thr  
                     185                      190                      195  
 30 His Leu Asn Asp Ile Val Pro Arg Val Pro Pro Met Asp Phe Gly Phe  
                     200                      205                      210  
 Ser Gln Pro Ser Pro Glu Tyr Trp Ile Thr Ser Gly Asn Gly Ala Ser  
     215                      220                      225  
 35  
 Val Thr Ala Ser Asp Ile Glu Val Ile Glu Gly Ile Asn Ser Thr Ala  
     230                      235                      240                      245  
 Gly Asn Ala Gly Glu Ala Thr Val Ser Val Val Ala His Leu Trp Tyr  
 40                      250                      255                      260  
 Phe Phe Ala Ile Ser Glu Cys Leu Leu \*  
                     265                      270